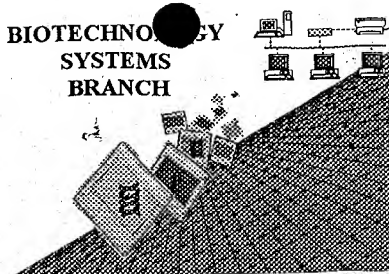


Forman

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/616,284
Source: 1600 RUSH
Date Processed by STIC: 8/6/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/6/6,284

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|--|---|
| 1 | _____ Wrapped Nucleic
Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." |
| 2 | _____ Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. |
| 3 | _____ Misaligned Amino
Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. |
| 4 | _____ Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. |
| 5 | _____ Variable Length | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. |
| 6 | _____ PatentIn 2.0
"bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 7 | _____ Skipped Sequences
(OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |
| 8 | _____ Skipped Sequences
(NEW RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 9 | _____ Use of n's or Xaa's
(NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 10 | _____ Invalid <213>
Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence |
| 11 | _____ Use of <220> | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) |
| 12 | _____ PatentIn 2.0
"bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. |

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/616,284

DATE: 08/06/2001
TIME: 11:45:48

Input Set : A:\NEX77CP2.txt
Output Set: N:\CRF3\08062001\I616284.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Gold, Larry
4 Zichi, Dominic A.
5 Jenison, Robert D.
6 Schneider, Daniel J.
8 <120> TITLE OF INVENTION: Method and Apparatus for the Automated Generation of
9 Nucleic Acid Ligands
11 <130> FILE REFERENCE: NEX77/CIP2
13 <140> CURRENT APPLICATION NUMBER: 09/616,284
14 <141> CURRENT FILING DATE: 2000-07-14
16 <150> PRIOR APPLICATION NUMBER: 09/356,233
17 <151> PRIOR FILING DATE: 1999-07-16
19 <150> PRIOR APPLICATION NUMBER: 09/232,946
20 <151> PRIOR FILING DATE: 1999-01-19
22 <150> PRIOR APPLICATION NUMBER: 08/792,075
23 <151> PRIOR FILING DATE: 1997-01-31
25 <150> PRIOR APPLICATION NUMBER: 09/143,190
26 <151> PRIOR FILING DATE: 1998-08-27
28 <150> PRIOR APPLICATION NUMBER: 08/469,609
29 <151> PRIOR FILING DATE: 1995-06-06
31 <150> PRIOR APPLICATION NUMBER: 07/714,131
32 <151> PRIOR FILING DATE: 1991-06-10
34 <150> PRIOR APPLICATION NUMBER: 07/536,428
35 <151> PRIOR FILING DATE: 1990-06-11
37 <160> NUMBER OF SEQ ID NOS: 5
39 <170> SOFTWARE: PatentIn Ver. 2.0
41 <210> SEQ ID NO: 1
42 <211> LENGTH: 43
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial Sequence *see item 11 on Ema Summary sheet*
46 <220> FEATURE:
47 <221> NAME/KEY: modified_base
48 <222> LOCATION: (1)..(43)
49 <223> OTHER INFORMATION: T at position 10 is substituted with DABCYL- (CH2)
50 6-; G at position 1 is substituted with 6-FAM.
52 <220> FEATURE:
53 <221> NAME/KEY: modified_base *duplicate above*
54 <222> LOCATION: (1)..(43)
55 <223> OTHER INFORMATION: T at position 10 is substituted with DABCYL- (CH2)
56 6-; G at position 1 is substituted with 6-FAM.
58 <400> SEQUENCE: 1
59 gagcgaagct ctaatacgcac tcactatagg gaggacgatg cgg 43
61 <210> SEQ ID NO: 2
62 <211> LENGTH: 51
63 <212> TYPE: DNA
64 <213> ORGANISM: Artificial Sequence *OK*
66 <220> FEATURE:
67 <221> NAME/KEY: modified_base

RAW SEQUENCE LISTING

DATE: 08/06/2001

PATENT APPLICATION: US/09/616,284

TIME: 11:45:48

Input Set : A:\NEX77CP2.txt

Output Set: N:\CRF3\08062001\I616284.raw

68 <222> LOCATION: (1)..(51)
 69 <223> OTHER INFORMATION: T at position 10 is substituted with DABCYL- (CH2)
 70 6-; G at position 1 is substituted with 6-FAM.
 72 <220> FEATURE:
 73 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 74 Sequence
 76 <400> SEQUENCE: 2
 77 gagcgaagct ctaatagcgc tcactatagg gagacaagaa taaacgctoa a 51
 79 <210> SEQ ID NO: 3
 80 <211> LENGTH: 61
 81 <212> TYPE: DNA
 82 <213> ORGANISM: Artificial Sequence
 84 <220> FEATURE:
 85 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 86 Sequence
 88 <220> FEATURE:
 89 <221> NAME/KEY: modified_base
 90 <222> LOCATION: (1)..(61)
 91 <223> OTHER INFORMATION: N at positions 16-45 is A, G, C or T.
 93 <400> SEQUENCE: 3
 94 gggaggacga tgcggnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnncagac gacgagcggg 60
 95 a 61
 97 <210> SEQ ID NO: 4
 98 <211> LENGTH: 23
 99 <212> TYPE: DNA
 100 <213> ORGANISM: Artificial Sequence
 102 <220> FEATURE:
 103 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 104 Sequence
 106 <400> SEQUENCE: 4
 107 atatatatgg gaggacgatg cgg 23
 109 <210> SEQ ID NO: 5
 110 <211> LENGTH: 24
 111 <212> TYPE: DNA
 112 <213> ORGANISM: Artificial Sequence
 114 <220> FEATURE:
 115 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 116 Sequence
 118 <400> SEQUENCE: 5
 119 tttttttttt ccgctcgtcg tctg 24

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/616,284

DATE: 08/06/2001

TIME: 11:45:49

Input Set : A:\NEX77CP2.txt

Output Set: N:\CRF3\08062001\I616284.raw

L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3